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<u>L8</u>	L7 not radio	6	<u>L8</u>
<u>L7</u>	l5 not radioactive	13	<u>L7</u>
<u>L6</u>	L5 same (advantag\$ or useful\$)	1	<u>L6</u>
<u>L5</u>	L3 same (bromine or iodine)	28	<u>L5</u>
<u>L4</u>	L3 same defect	6	<u>L4</u>
<u>L3</u>	L1 same mass same label\$	3640	<u>L3</u>
<u>L2</u>	L1 same (mass near0 defect)	0	<u>L2</u>
<u>L1</u>	oligomer or oligonucleotide or polynucleotide or DNA or RNA or protein or lipid	192712	<u>L1</u>

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L6	L2 same label\$ same fragment	7	L6
L5	L2 same label\$ same oligomer	0	L5
L4	L2 same label\$ oligomer	45788	L4
L3	L2 same (label\$ near0 oligomer)	0	L3
L2	L1 same identif\$	1075	L2
L1	mass near0 spectrum	13100	L1

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=> s mass(wdefect
MISSING OPERATOR 'MASS(WDEFECT'
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nested terms that are not separated by a logical operator.

=> s mass(w)defect
L1 378 MASS(W) DEFECT

=> s l1(p)label?
L2 3 L1(P) LABEL?

=> d bib ab l2 1-3

L2 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2002:658346 CAPLUS

DN 137:165811

TI **Mass defect labeling** for the determination
of oligomer sequences

IN Schneider, Luke V.; Hall, Michael P.; Petesch, Robert

PA Target Discovery, Inc, USA

SO PCT Int. Appl., 123 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002066952	A2	20020829	WO 2001-US49951	20011019
	WO 2002066952	A3	20030904		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,
PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2002172961	A1	20021121	US 2001-35349	20011019
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PRAI US 2000-242165P P 20001019

US 2000-242398P P 20001019

AB The invention concerns mass tagging methods are provided that lead to mass spectrometer detection sensitivities and mol. discriminations that are improved over other methods. In particular the methods are useful for discriminating tagged mols. and fragments of mols. from chem. noise in the mass spectrum. These mass tagging methods are useful for oligomer sequencing, detg. the relative abundances of mols. from different samples, and identifying individual mols. or chem. processing steps in combinatorial chem. libraries. The methods provided are useful for the simultaneous anal. of multiple mols. and reaction mixts. by mass

spectrometric methods.

L2 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2002:595153 CAPLUS
DN 137:152020
TI Mass spectrometric methods for determining terminal oligomer sequences in
proteins and nucleic acids and oligosaccharides and lipids
IN Schneider, Luke V.; Petesch, Robert; Hall, Michael P.
PA Target Discovery, Inc., USA
SO PCT Int. Appl., 151 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 2002061661	A2	20020808	WO 2001-US49491	20011019
	W:				
	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,				
	CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,				
	GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,				
	LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,				
	PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,				
	UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW:				
	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,				
	DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,				
	BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2002172961	A1	20021121	US 2001-35349	20011019
PRAI	US 2000-242165P	P	20001019		
	US 2000-242398P	P	20001019		

AB Methods and app. are provided for deriving the sequence of an oligomer, and in particular a terminal portion of an oligomer **labeled** with a **mass defect label**. A math. algorithm is provided for detg. a protein sequence tag directly from mass spectra of fragmented **labeled** proteins. The algorithm requires the use of both the mass-to-charge position of a signal and its relative abundance, and further consists of a cumulative sequence ranking system in which the relative abundance of the ions predicted to result from each possible sequence are combined by product or summation with the relative abundances of ions predicted to result from subsequent residues. Thus, in one exemplary method for deriving the sequence of a polypeptide, a predetd. set of mass/charge values for amino acid sequences is stored. An abundance value from mass spectrum data for each mass/charge value in the predetd. set is detd. to produce a plurality of abundance values. A first ranking, based on the plurality of abundance values, is calcd. for each sequence of a set of amino acid sequences having a first no. of amino acids. A second ranking, based on the plurality of abundance values, for each sequence of a set of amino acid sequences having a second no. of amino acids is calcd. A cumulative ranking, based on the first ranking and the second ranking, is calcd. for each sequence of a set of amino acid sequences having at least the second no. of amino acids. The method is also exemplified for the sequence anal. of nucleic acids and oligosaccharides, and for identification of fatty acid compn. and arrangement in lipids (lipid sequencing). A no. of photocleavable **mass defect labels** are described.

L2 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1980:31407 CAPLUS
DN 92:31407
TI Rearrangement of a vibrational spectrum of a crystal in the presence of
impurity states of a large radius
AU Ivanov, M. A.; Pogorelov, Yu. G.
CS Inst. Metallofiz., Kiev, USSR
SO Fizika Nizkikh Temperatur (Kiev) (1979), 5(8), 910-24

CODEN: FNTEDK; ISSN: 0132-6414

DT Journal

LA Russian

AB The phonon spectrum of a crystal contg. impurities is considered, both the **mass defect** and the change in force consts. being taken into account. In the system contg. long range impurity states a small characteristic concn. of impurities exists at which the spectrum is essentially redistributed near the impurity mode frequency. Two kinds of possible rearrangement (coherent and incoherent) are found. For low-frequency quasilocal vibrations the rearrangement (coherent and incoherent) are found. For low-frequency quasilocal vibrations the rearrangement is always coherent and the spectrum is cross splitted. When the impurity level is close to the optical band edge (or to the top of the acoustic band) both types of rearrangement can occur depending on the relation between the perturbation parameters. With low impurity concns., a new (impurity) band where the states are crystal momentum **labeled** could appear provided that the impurities are weakly bound and light. An influence of the coherent rearrangement on the character of the optical spectra of impurity states is discussed.

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L1 378 S MASS(W)DEFECT

L2 3 S L1(P)LABEL?